



SEQUENCE LISTING

<110> Porro, Danilo
 Branduardi, Paola
 Valli, Minoska
 Alberghina, Lilia

<120> Process for Expression and Secretion of
 Proteins by the Non-Conventional Yeast Zygosaccharomyces
 Bailii

<130> 3912.1000-000

<140> 10/534,171

<141> 2005-05-06

<150> PCT/EP2003/012377

<151> 2003-11-06

<150> 102 52 245.6

<151> 2002-11-07

<160> 95

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 gtgcaagaaa accaaaaagc aacaacaggt tttggataag tacatatata agagggcctt 180
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 Ile Pro Ala Glu Ala Val Ile Gly Tyr Leu Asp Leu Glu Gly Asp Phe
 -50 -45 -40
 Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
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 Ser Leu Asp Lys Arg
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<210> 5
 <211> 63
 <212> DNA
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<220>
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<210> 6
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 <213> *Aspergillus niger*

<220>
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 <222> (1)...(21)

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 <213> Bacillus sp.

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 <222> (1)...(17)

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<210> 17
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<210> 20
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 <212> DNA
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<210> 22
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<220>
<221> SIGNAL
<222> (1)...(18)

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<210> 23
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<212> DNA
<213> Homo sapiens

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<210> 24
<211> 19
<212> PRT
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<222> (1)...(19)

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<210> 25
<211> 75
<212> DNA
<213> Rhizopus oryzae

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<222> (1)...(75)

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<210> 26
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<212> PRT
<213> Rhizopus oryzae

<220>
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 <222> (1)...(25)

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<210> 27
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<210> 29
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<210> 30
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<212> PRT

<213> *Saccharomyces cerevisiae*

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<221> SIGNAL

<222> (1)...(26)

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<210> 33

<211> 63

<212> DNA

<213> *Saccharomyces cerevisiae*

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<221> sig_peptide

<222> (1)...(63)

<400> 33

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<210> 34

<211> 21

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> SIGNAL

<222> (1)...(21)

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-5

<210> 35

<211> 48

<212> DNA

<213> Kluyveromyces lactis

<220>

<221> sig_peptide

<222> (1)...(48)

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48

<210> 36

<211> 17

<212> PRT

<213> Kluyveromyces lactis

<220>

<221> SIGNAL

<222> (1)...(17)

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Leu

<210> 37

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<212> DNA

<213> Kluyveromyces lactis

<220>

<221> sig_peptide

<222> (1)...(69)

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<213> Kluyveromyces lactis

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<221> SIGNAL

<222> (1)...(23)

* <400> 38

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<210> 39

<211> 54

<212> DNA

<213> *Saccharomyces cerevisiae*

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<222> (1)...(54)

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<211> 18

<212> PRT

<213> *Saccharomyces cerevisiae*

<220>

<221> SIGNAL

<222> (1)...(18)

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<210> 41

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<213> *Saccharomyces cerevisiae*

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<222> (1)...(54)

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<220>

<221> SIGNAL

<222> (1)...(18)

<400> 42

12/31

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 <222> (1)...(17)

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<210> 45
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 <222> (1)...(48)

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<210> 46
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-15

-10

-5

<210> 47
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<210> 49
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 <212> DNA
 <213> Aspergillus niger

<220>
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 <212> PRT
 <213> Aspergillus niger

<220>
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<210> 51
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 <212> DNA
 <213> *Saccharomyces cerevisiae*

<220>
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 <222> (1)...(57)

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<220>
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<210> 53
 <211> 63
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 <213> *Saccharomyces cerevisiae*

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 <222> (1)...(63)

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 ggt 63

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 <213> *Saccharomyces cerevisiae*

<220>
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 <222> (1)...(21)

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 Asn Ser Ala Leu Gly
 -5

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 <213> *Saccharomyces cerevisiae*

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 ggt 63

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 <213> *Saccharomyces cerevisiae*

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 <212> DNA
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 <213> *Saccharomyces cerevisiae*

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 -15 -10 -5

<210> 59
 <211> 63
 <212> DNA
 <213> Zygosaccharomyces bailii

<220>
 <221> sig_peptide
 <222> (1)...(63)

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 gct 63

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 <213> Zygosaccharomyces bailii

<220>
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 <222> (1)...(21)

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 <213> Zygosaccharomyces bailii

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 <222> (1)...(417)

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 gaagaaattt ttacagattt gacgtatcac attcacgtta acgtcagtg cgaaattgac 180
 tcttactatc ataatttagt caattttgtc gataacgctc tagcaaaca agatattaat 240
 agatatatat acgctatat tacacagcag acaaaactata cagaggatgg gctcattgag 300
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<220>
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 Glu Leu Lys Thr Ala Phe Gly Asp Glu Glu Ile Phe Thr Asp Leu Thr
 -105 -100 -95
 Tyr His Ile His Val Asn Val Ser Gly Glu Ile Asp Ser Tyr Tyr His
 -90 -85 -80
 Asn Leu Val Asn Phe Val Asp Asn Ala Leu Ala Asn Lys Asp Ile Asn
 -75 -70 -65 -60
 Arg Tyr Ile Tyr Ala Ile Phe Thr Gln Gln Thr Asn Tyr Thr Glu Asp
 -55 -50 -45
 Gly Leu Ile Glu Tyr Leu Asn His Tyr Asp Ser Glu Thr Cys Lys Asp
 -40 -35 -30
 Ile Ile Thr Gln Tyr Asn Val Asn Val Asp Thr Ser Asn Cys Ile Ser
 -25 -20 -15
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 -10 -5

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<212> DNA

<213> Zygosaccharomyces bailii

<400> 63

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taactcaagg gggagtagtt ttgaggatca catgggaagt atttaaataa atagtagttc 180
ttttgtttta aaaaggcctc tccaaaagta atacttttag ggtaattact aagtataata 240
tatattataa gtaatagcct ttatagctta atggtaaagc agtaaattga agatttacct 300
atatgtagtt cgattctcat taagggaat ataaataagc tttttaatgg gccaatagct 360
gaaataagta atattattgt aaatattgag acttgaactc aaatcctatg cacctaaaaa 420
catatatatt aaccaattaa attatatatta ctttattatt tacttatata acttctacta 480
attgtaaagt ataaccagct tttttgttaa caacaaaaac cgagagggtt catgttatat 540
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<210> 64

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<212> DNA

<213> Zygosaccharomyces bailii

<400> 64

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ccccctatga gttttcatat tataaatata aaaactttta tggagggacc tataagaaat 180
aattgaggaa taattaataa taagttgccc tccttttttt tctcttctcc ccaccctaaa 240
aatactcctg ggggggggag ggagagaatg tatgtagtgg ggagggtgta agttaataat 300
agacttaaag agagttatat aaaataacat aaatatgctt aaaaataata ataataatat 360
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atctatccta tctga 435

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<210> 65

<211> 299

<212> DNA

<213> Zygosaccharomyces bailii

<400> 65

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cgggcgctag ggcgctggca agtgtagcgg tcacgctgcg cgtaaccacc acaccgccg 180
cgcttaatgc gccgctacag ggcgcgtcag gtggcacttt tcgggggaaat gtgcgcggaa 240
cccctatttg tttatttttc taaatacatt caaatatgta tccgctcatg agacaataa 299

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<210> 66

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<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 66

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gttattcctc tctccagagt caggcttctg tgt 153

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<210> 67

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<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 67

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tctggagatt ttgcataaac aactgattta ttattagctt tatttttctaa tccattaact 120
aattgatcat acataatata gatgaataag aataatgaaa ctagtgcaat aattgatcca 180
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<210> 68

<211> 52

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 68

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<210> 69

<211> 116

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 69

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<210> 70

<211> 268

<212> DNA

<213> *Zygosaccharomyces bailii*

<400> 70

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cctgggcata attgagcaaa tcgtactcgt gcgcggcgat gcgctccttg ccgatcgaat 120
tgacgtaatc gatcgcgggcg ccgagcccga tcgcctcgac gatcgggcggc gtgccggcct 180
cgaacttgtg cggcggggtcg ccataggtga cccagtcctt ggcaacttca cggatcattt 240
cgccgcccgc gttgaacggc cgcacgcg 268

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<210> 71
 <211> 869
 <212> DNA
 <213> *Zygosaccharomyces bailii*

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 tcggtaccac gcatgctgca gacgcgttac gtatcggatc cagaattcgt gatattctat 120
 tgggtatgtc ccctgattcg acggcgtaaa ttgctggaat cttgtgttgg cgctaatagac 180
 cgcttttttg aattatgtgc tatgcctctg ccattgggat caacagctga aatattttgtt 240
 gaagatcgaa tatcttctat tgtttctgag ggtatccccg aagctatggc gaaagaaagg 300
 atctcttctc gtacttggat cggtagcaga agcaatagac gcacaatgca ttgacgcatac 360
 ttgttgatac cgggtaaatgt gagtcttctg ggttctgtta ttgagttaa tatgtcgtcc 420
 acctctgttc tcgtatccat tttgcgagta gcccgccata cagcacgtcc aatacaggag 480
 aggccattta gcttcagggtg cagagaagac acagcatggt gctcaccttc gagtgtctca 540
 atagatgatt gagttgactg ggcttccgtg aaagggcctt tcgagagatc ttcagaaata 600
 aaccagggtt gcgcttcatt agtaggtgtt cctggaggac tattgtcgtc atctgctgga 660
 ctactgctac caagtagtga aggggggtatt ctaaggcttt cactctgttc tgacactatt 720
 ataacattgc caaggccaat ttgaaagggt tcgcgtatat gagtaaagag ctcggtgcc 780
 ttccagttgg aatcaagccg ttcaagcaga tcgagagcat aatcagagtc cacatttccg 840
 cagcaagag agaactctga gttcattct 869

<210> 72
 <211> 1425
 <212> DNA
 <213> *Zygosaccharomyces bailii*

<220>
 <221> CDS
 <222> (1)...(1425)

<400> 72
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 Met Ser Glu Phe Ser Glu Leu Val Arg Ile Leu Pro Leu Asp Gln Val
 1 5 10 15
 gca gaa ata aag cgt att ttg agt cgc ggc gac cct ata cct tta caa 96
 Ala Glu Ile Lys Arg Ile Leu Ser Arg Gly Asp Pro Ile Pro Leu Gln
 20 25 30
 agg tta gct tct cta cta act atg gtg atc cta acg gtc aac atg tca 144
 Arg Leu Ala Ser Leu Leu Thr Met Val Ile Leu Thr Val Asn Met Ser
 35 40 45
 aaa aag agg aag agc tct cca atc aag ctt agc acc ttt act aaa tat 192
 Lys Lys Arg Lys Ser Ser Pro Ile Lys Leu Ser Thr Phe Thr Lys Tyr
 50 55 60
 cgt aga aat gtt gcg aag tca ttg tat tat gat atg tca agc aag aca 240
 Arg Arg Asn Val Ala Lys Ser Leu Tyr Tyr Asp Met Ser Ser Lys Thr
 65 70 75 80
 gta ttc ttc gaa tac cat ctc aaa aat aca caa gat cta cag gag ggc 288
 Val Phe Phe Glu Tyr His Leu Lys Asn Thr Gln Asp Leu Gln Glu Gly
 85 90 95
 ctc gag caa gcc att gcg ccc tac aat ttc gtg gta aag gtg cac aag 336

Leu	Glu	Gln	Ala	Ile	Ala	Pro	Tyr	Asn	Phe	Val	Val	Lys	Val	His	Lys	
			100					105					110			
aag	cca	att	gat	tgg	cag	aaa	cag	ctc	tca	agc	gtg	cat	gag	agg	aaa	384
Lys	Pro	Ile	Asp	Trp	Gln	Lys	Gln	Leu	Ser	Ser	Val	His	Glu	Arg	Lys	
		115					120					125				
gcg	ggc	cac	aga	agc	att	ctc	agc	aac	aat	gtt	ggc	gcc	gag	atc	tct	432
Ala	Gly	His	Arg	Ser	Ile	Leu	Ser	Asn	Asn	Val	Gly	Ala	Glu	Ile	Ser	
	130					135					140					
aaa	ctg	gct	gag	acg	aaa	gat	tct	act	tgg	agt	ttt	atc	gag	aga	aca	480
Lys	Leu	Ala	Glu	Thr	Lys	Asp	Ser	Thr	Trp	Ser	Phe	Ile	Glu	Arg	Thr	
145					150				155						160	
atg	gat	ctg	ata	gaa	gcc	cgc	acc	cgc	cag	ccc	acg	aca	aga	gtt	gcg	528
Met	Asp	Leu	Ile	Glu	Ala	Arg	Thr	Arg	Gln	Pro	Thr	Thr	Arg	Val	Ala	
				165					170					175		
tat	agg	ttt	ctg	ctt	caa	ctc	aca	ttc	atg	aac	tgc	tgt	agg	gct	aat	576
Tyr	Arg	Phe	Leu	Leu	Gln	Leu	Thr	Phe	Met	Asn	Cys	Cys	Arg	Ala	Asn	
			180					185					190			
gat	ttg	aaa	aac	gcc	gac	ccc	agc	act	ttt	caa	atc	atc	gca	gat	cct	624
Asp	Leu	Lys	Asn	Ala	Asp	Pro	Ser	Thr	Phe	Gln	Ile	Ile	Ala	Asp	Pro	
		195					200					205				
cac	ctt	ggc	cgt	ata	ttg	cgg	gcc	ttt	gtt	cca	gag	aca	aag	act	agc	672
His	Leu	Gly	Arg	Ile	Leu	Arg	Ala	Phe	Val	Pro	Glu	Thr	Lys	Thr	Ser	
	210					215					220					
att	gaa	agg	ttt	atc	tat	ttt	ttc	cca	tgt	aag	gga	cga	tgc	gat	ccg	720
Ile	Glu	Arg	Phe	Ile	Tyr	Phe	Phe	Pro	Cys	Lys	Gly	Arg	Cys	Asp	Pro	
225					230				235						240	
ctt	ttg	gct	cta	gat	tcc	tat	ctc	ctg	tgg	gtt	ggc	cca	gtg	ccc	aaa	768
Leu	Leu	Ala	Leu	Asp	Ser	Tyr	Leu	Leu	Trp	Val	Gly	Pro	Val	Pro	Lys	
				245					250					255		
act	cag	act	acc	gat	gaa	gag	act	caa	tat	gat	tac	cag	ctt	ctt	caa	816
Thr	Gln	Thr	Thr	Asp	Glu	Glu	Thr	Gln	Tyr	Asp	Tyr	Gln	Leu	Leu	Gln	
			260					265					270			
gat	act	ctc	ttg	att	tcg	tac	gac	agg	ttt	atc	gcc	aaa	gaa	tca	aag	864
Asp	Thr	Leu	Leu	Ile	Ser	Tyr	Asp	Arg	Phe	Ile	Ala	Lys	Glu	Ser	Lys	
		275					280					285				
gaa	aat	att	ttc	aaa	ata	cct	aat	ggg	ccc	aaa	gct	cat	ttg	ggg	cgg	912
Glu	Asn	Ile	Phe	Lys	Ile	Pro	Asn	Gly	Pro	Lys	Ala	His	Leu	Gly	Arg	
	290					295					300					
cat	cta	atg	gca	tca	tac	ctt	gga	aac	aac	agt	ctc	aag	agc	gag	gcc	960
His	Leu	Met	Ala	Ser	Tyr	Leu	Gly	Asn	Asn	Ser	Leu	Lys	Ser	Glu	Ala	
305					310					315					320	
aca	ctc	tac	ggc	aac	tgg	tct	gtg	gaa	agg	caa	gag	ggc	gtc	agc	aaa	1008
Thr	Leu	Tyr	Gly	Asn	Trp	Ser	Val	Glu	Arg	Gln	Glu	Gly	Val	Ser	Lys	

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325										330					335					
atg	gct	gac	agc	cga	tac	atg	cac	acg	gtt	aaa	aaa	agt	cca	cct	tca	1056				
Met	Ala	Asp	Ser	Arg	Tyr	Met	His	Thr	Val	Lys	Lys	Ser	Pro	Pro	Ser					
			340						345				350							
tat	cta	ttt	gca	ttt	tta	tcc	ggc	tac	tac	aaa	aag	tcc	aac	caa	ggc	1104				
Tyr	Leu	Phe	Ala	Phe	Leu	Ser	Gly	Tyr	Tyr	Lys	Lys	Ser	Asn	Gln	Gly					
		355					360					365								
gag	tac	gtg	ctg	gct	gaa	aca	ctg	tat	aat	ccc	ctg	gat	tac	gac	aaa	1152				
Glu	Tyr	Val	Leu	Ala	Glu	Thr	Leu	Tyr	Asn	Pro	Leu	Asp	Tyr	Asp	Lys					
	370					375					380									
aca	ctt	cca	ata	aca	acg	aac	gag	aaa	ttg	atc	tgt	cgg	cgg	tac	ggg	1200				
Thr	Leu	Pro	Ile	Thr	Thr	Asn	Glu	Lys	Leu	Ile	Cys	Arg	Arg	Tyr	Gly					
385					390					395					400					
aaa	aat	gcg	aaa	gtg	ata	cca	aaa	gac	gca	ctg	ctg	tat	ctc	tac	acg	1248				
Lys	Asn	Ala	Lys	Val	Ile	Pro	Lys	Asp	Ala	Leu	Leu	Tyr	Leu	Tyr	Thr					
				405					410					415						
tat	gcg	cag	cag	aag	cga	aaa	caa	ttg	gcc	gat	ccc	aat	gag	caa	aat	1296				
Tyr	Ala	Gln	Gln	Lys	Arg	Lys	Gln	Leu	Ala	Asp	Pro	Asn	Glu	Gln	Asn					
			420					425					430							
agg	cta	ttc	agt	agt	gaa	tca	cca	gcg	cat	ccc	ttc	tta	act	cct	caa	1344				
Arg	Leu	Phe	Ser	Ser	Glu	Ser	Pro	Ala	His	Pro	Phe	Leu	Thr	Pro	Gln					
		435					440					445								
tcg	aca	ggc	tca	tcg	aca	ccc	ttg	acc	tgg	act	gct	cca	aag	aca	ctc	1392				
Ser	Thr	Gly	Ser	Ser	Thr	Pro	Leu	Thr	Trp	Thr	Ala	Pro	Lys	Thr	Leu					
	450					455					460									
tcc	act	ggt	cta	atg	aca	cct	gga	gaa	gag	tag						1425				
Ser	Thr	Gly	Leu	Met	Thr	Pro	Gly	Glu	Glu	*										
465					470															

<210> 73

<211> 474

<212> PRT

<213> Zygosaccharomyces bailii

<400> 73

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Ala	Glu	Ile	Lys	Arg	Ile	Leu	Ser	Arg	Gly	Asp	Pro	Ile	Pro	Leu	Gln
			20					25					30		
Arg	Leu	Ala	Ser	Leu	Leu	Thr	Met	Val	Ile	Leu	Thr	Val	Asn	Met	Ser
			35				40					45			
Lys	Lys	Arg	Lys	Ser	Ser	Pro	Ile	Lys	Leu	Ser	Thr	Phe	Thr	Lys	Tyr
	50					55					60				
Arg	Arg	Asn	Val	Ala	Lys	Ser	Leu	Tyr	Tyr	Asp	Met	Ser	Ser	Lys	Thr
65					70					75					80
Val	Phe	Phe	Glu	Tyr	His	Leu	Lys	Asn	Thr	Gln	Asp	Leu	Gln	Glu	Gly
				85					90					95	

<220>
<221> CDS

<222> (1)...(1074)

<400> 74

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1				5					10					15		
aag	atg	atc	ttt	gat	gtg	ctt	atg	aca	ttt	cct	tac	ttc	gcg	gta	cat	96
Lys	Met	Ile	Phe	Asp	Val	Leu	Met	Thr	Phe	Pro	Tyr	Phe	Ala	Val	His	
			20					25					30			
gtt	cct	tcc	aag	aat	ata	ctt	atc	aca	cca	aaa	ggc	aca	gtt	gag	ata	144
Val	Pro	Ser	Lys	Asn	Ile	Leu	Ile	Thr	Pro	Lys	Gly	Thr	Val	Glu	Ile	
			35				40					45				
cct	gaa	aac	tat	caa	aat	tat	ccc	ata	ttg	gcc	atc	ttc	tac	gtc	aaa	192
Pro	Glu	Asn	Tyr	Gln	Asn	Tyr	Pro	Ile	Leu	Ala	Ile	Phe	Tyr	Val	Lys	
	50					55					60					
tat	tta	atg	aag	aaa	aat	ccg	tac	gat	ctt	ctt	cca	agc	acc	gtg	aac	240
Tyr	Leu	Met	Lys	Lys	Asn	Pro	Tyr	Asp	Leu	Leu	Pro	Ser	Thr	Val	Asn	
65					70					75					80	
tgg	ccg	gaa	ccc	tat	gta	gtg	gtg	aat	acc	atc	act	aag	cgt	ttc	cag	288
Trp	Pro	Glu	Pro	Tyr	Val	Val	Val	Asn	Thr	Ile	Thr	Lys	Arg	Phe	Gln	
				85					90					95		
gac	cat	aaa	cta	ttt	gca	aac	aaa	aat	gct	gat	gtc	tac	gtt	gaa	aga	336
Asp	His	Lys	Leu	Phe	Ala	Asn	Lys	Asn	Ala	Asp	Val	Tyr	Val	Glu	Arg	
			100					105					110			
ctt	caa	aat	gca	att	gcc	tcg	ggc	att	aag	att	cct	gag	tct	aag	aag	384
Leu	Gln	Asn	Ala	Ile	Ala	Ser	Gly	Ile	Lys	Ile	Pro	Glu	Ser	Lys	Lys	
		115					120					125				
aat	gaa	cga	tta	ggg	cag	cca	aaa	aag	acg	aaa	aat	gtt	aca	aaa	gag	432
Asn	Glu	Arg	Leu	Gly	Gln	Pro	Lys	Lys	Thr	Lys	Asn	Val	Thr	Lys	Glu	
	130					135					140					
aat	tga	gga	gac	ctt	tat	tga	tgc	cac	taa	tgc	gag	aaa	aga	att	gga	480
Asn	*	Gly	Asp	Leu	Tyr	*	Cys	His	*	Cys	Glu	Lys	Arg	Ile	Gly	
145							150						155			
tga	gta	ctt	cag	aaa	act	tca	gga	tgg	tac	att	aac	cgg	aga	ttt	gga	528
*	Val	Leu	Gln	Lys	Thr	Ser	Gly	Trp	Tyr	Ile	Asn	Arg	Arg	Phe	Gly	
			160					165					170			
ggg	tgg	ctt	gtg	caa	ggc	caa	aac	gct	cat	atc	gtg	taa	agc	ttt	gtt	576
Gly	Trp	Leu	Val	Gln	Gly	Gln	Asn	Ala	His	Ile	Val	*	Ser	Phe	Val	
		175					180						185			
cgg	agg	aca	cac	cca	aga	act	cca	gtt	tat	ggc	cac	caa	tgt	tcg	taa	624
Arg	Arg	Thr	His	Pro	Arg	Thr	Pro	Val	Tyr	Gly	His	Gln	Cys	Ser	*	
		190					195					200				
agt	ctg	gat	agg	gga	gat	agt	gtg	cgg	cat	ggc	ttc	caa	taa	aaa	tgc	672
Ser	Leu	Asp	Arg	Gly	Asp	Ser	Val	Arg	His	Gly	Phe	Gln	*	Lys	Cys	

205					210					215						
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Asn	*	Arg	*	*	Ser	Arg	Gly	Arg	Arg	Ala	*	Cys	Ile	Gly	Arg	
					220					225						
aca	aac	tac	gac	agc	ccg	aga	gga	atc	aga	ggc	tct	gga	tac	cac	atc	768
Thr	Asn	Tyr	Asp	Ser	Pro	Arg	Gly	Ile	Arg	Gly	Ser	Gly	Tyr	His	Ile	
230					235					240					245	
caa	tgg	ttt	gga	cgc	tct	gaa	tac	tca	aat	taa	tgc	cat	aga	aac	gga	816
Gln	Trp	Phe	Gly	Arg	Ser	Glu	Tyr	Ser	Asn	*	Cys	His	Arg	Asn	Gly	
				250					255						260	
gga	atc	att	ttg	gga	agc	tat	cag	ggc	gct	cca	taa	tga	gct	acg	cac	864
Gly	Ile	Ile	Leu	Gly	Ser	Tyr	Gln	Gly	Ala	Pro	*	*	Ala	Thr	His	
				265					270							
ctc	tcc	aac	aca	gtt	aga	aga	gtg	cag	gaa	agc	ggc	agt	ttt	ttt	act	912
Leu	Ser	Asn	Thr	Val	Arg	Arg	Val	Gln	Glu	Ser	Gly	Ser	Phe	Phe	Thr	
275					280					285					290	
ggg	cca	taa	aaa	aat	act	cca	aac	att	tac	aaa	gca	aaa	gga	tac	tgc	960
Gly	Pro	*	Lys	Asn	Thr	Pro	Asn	Ile	Tyr	Lys	Ala	Lys	Gly	Tyr	Cys	
					295					300					305	
ccg	cgc	tct	ttt	tta	tat	aaa	tct	caa	aga	gtg	tct	ggg	aac	cag	ctg	1008
Pro	Arg	Ser	Phe	Leu	Tyr	Lys	Ser	Gln	Arg	Val	Ser	Gly	Asn	Gln	Leu	
				310					315					320		
gaa	ttt	aga	ata	tac	aga	ggc	atc	aga	tgc	aag	aaa	aat	ggc	aat	taa	1056
Glu	Phe	Arg	Ile	Tyr	Arg	Gly	Ile	Arg	Cys	Lys	Lys	Asn	Gly	Asn	*	
			325					330					335			
agg	tga	gct	tca	aaa	tta	a										1075
Arg	*	Ala	Ser	Lys	Leu											
				340												

<210> 75

<211> 341

<212> PRT

<213> Zygosaccharomyces bailii

<400> 75

Met	Phe	Ser	Arg	Glu	Glu	Val	Arg	Ala	Ser	Arg	Pro	Thr	Lys	Glu	Met	
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Lys	Met	Ile	Phe	Asp	Val	Leu	Met	Thr	Phe	Pro	Tyr	Phe	Ala	Val	His	
			20					25					30			
Val	Pro	Ser	Lys	Asn	Ile	Leu	Ile	Thr	Pro	Lys	Gly	Thr	Val	Glu	Ile	
			35				40					45				
Pro	Glu	Asn	Tyr	Gln	Asn	Tyr	Pro	Ile	Leu	Ala	Ile	Phe	Tyr	Val	Lys	
	50					55					60					
Tyr	Leu	Met	Lys	Lys	Asn	Pro	Tyr	Asp	Leu	Leu	Pro	Ser	Thr	Val	Asn	
65					70				75						80	
Trp	Pro	Glu	Pro	Tyr	Val	Val	Val	Asn	Thr	Ile	Thr	Lys	Arg	Phe	Gln	
				85					90					95		

Asp	His	Lys	Leu	Phe	Ala	Asn	Lys	Asn	Ala	Asp	Val	Tyr	Val	Glu	Arg	
			100					105					110			
Leu	Gln	Asn	Ala	Ile	Ala	Ser	Gly	Ile	Lys	Ile	Pro	Glu	Ser	Lys	Lys	
		115					120					125				
Asn	Glu	Arg	Leu	Gly	Gln	Pro	Lys	Lys	Thr	Lys	Asn	Val	Thr	Lys	Glu	
		130				135					140					
Asn	Gly	Asp	Leu	Tyr	Cys	His	Cys	Glu	Lys	Arg	Ile	Gly	Val	Leu	Gln	
					150					155					160	
Lys	Thr	Ser	Gly	Trp	Tyr	Ile	Asn	Arg	Arg	Phe	Gly	Gly	Trp	Leu	Val	
				165					170					175		
Gln	Gly	Gln	Asn	Ala	His	Ile	Val	Ser	Phe	Val	Arg	Arg	Thr	His	Pro	
			180					185					190			
Arg	Thr	Pro	Val	Tyr	Gly	His	Gln	Cys	Ser	Ser	Leu	Asp	Arg	Gly	Asp	
		195					200					205				
Ser	Val	Arg	His	Gly	Phe	Gln	Lys	Cys	Asn	Arg	Ser	Arg	Gly	Arg	Arg	
		210				215					220					
Ala	Cys	Ile	Gly	Arg	Thr	Asn	Tyr	Asp	Ser	Pro	Arg	Gly	Ile	Arg	Gly	
					230					235					240	
Ser	Gly	Tyr	His	Ile	Gln	Trp	Phe	Gly	Arg	Ser	Glu	Tyr	Ser	Asn	Cys	
				245					250					255		
His	Arg	Asn	Gly	Gly	Ile	Ile	Leu	Gly	Ser	Tyr	Gln	Gly	Ala	Pro	Ala	
			260					265					270			
Thr	His	Leu	Ser	Asn	Thr	Val	Arg	Arg	Val	Gln	Glu	Ser	Gly	Ser	Phe	
		275					280					285				
Phe	Thr	Gly	Pro	Lys	Asn	Thr	Pro	Asn	Ile	Tyr	Lys	Ala	Lys	Gly	Tyr	
		290				295					300					
Cys	Pro	Arg	Ser	Phe	Leu	Tyr	Lys	Ser	Gln	Arg	Val	Ser	Gly	Asn	Gln	
					310					315					320	
Leu	Glu	Phe	Arg	Ile	Tyr	Arg	Gly	Ile	Arg	Cys	Lys	Lys	Asn	Gly	Asn	
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Arg	Ala	Ser	Lys	Leu												
			340													

<210> 76

<211> 750

<212> DNA

<213> Zygosaccharomyces bailii

<220>

<221> CDS

<222> (1)...(750)

<400> 76

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Met	Asn	Ser	Glu	Phe	Ser	Leu	Ala	Tyr	Gly	Asn	Val	Asp	Ser	Asp	Tyr	
1				5					10					15		

gct	ctc	gat	ctg	ctt	gaa	cgg	ctt	gat	tcc	aac	tgg	aag	ggc	acc	gag	96
Ala	Leu	Asp	Leu	Leu	Glu	Arg	Leu	Asp	Ser	Asn	Trp	Lys	Gly	Thr	Glu	
			20					25					30			

ctc	ttt	act	cat	ata	cgc	gaa	acc	ttt	caa	att	ggc	ctt	ggc	aat	gtt	144
Leu	Phe	Thr	His	Ile	Arg	Glu	Thr	Phe	Gln	Ile	Gly	Leu	Gly	Asn	Val	
		35					40					45				

atc	ata	gtg	tca	gaa	cag	agt	gaa	agc	ctt	aga	ata	ccc	cct	tca	cta	192
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Ile	Ile	Val	Ser	Glu	Gln	Ser	Glu	Ser	Leu	Arg	Ile	Pro	Pro	Ser	Leu		
50						55					60						
ctt	ggt	agc	agt	agt	cca	gca	gat	agc	gac	aat	agt	cct	cca	gga	aca	240	
Leu	Gly	Ser	Ser	Ser	Pro	Ala	Asp	Ser	Asp	Asn	Ser	Pro	Pro	Gly	Thr	80	
65					70					75							
cct	act	aat	gaa	gcg	caa	ccc	tgg	ttt	att	tct	gaa	gat	ctc	tcg	aaa	288	
Pro	Thr	Asn	Glu	Ala	Gln	Pro	Trp	Phe	Ile	Ser	Glu	Asp	Leu	Ser	Lys	95	
				85					90								
ggc	cct	ttc	acg	gaa	gcc	cag	tca	act	caa	tca	tct	att	gag	aca	ctc	336	
Gly	Pro	Phe	Thr	Glu	Ala	Gln	Ser	Thr	Gln	Ser	Ser	Ile	Glu	Thr	Leu	110	
			100					105									
gaa	ggt	gag	cac	cat	gct	gtg	tct	tct	ctg	cac	ctg	aag	cta	aat	ggc	384	
Glu	Gly	Glu	His	His	Ala	Val	Ser	Ser	Leu	His	Leu	Lys	Leu	Asn	Gly	125	
		115					120					125					
ctc	tcc	tgt	att	gga	cgt	gct	gta	tgg	cgg	gct	act	cgc	aaa	atg	gat	432	
Leu	Ser	Cys	Ile	Gly	Arg	Ala	Val	Trp	Arg	Ala	Thr	Arg	Lys	Met	Asp	140	
	130					135					140						
acg	aga	aca	gag	gtg	gac	gac	ata	tta	aac	tca	ata	aca	gaa	ccc	aga	480	
Thr	Arg	Thr	Glu	Val	Asp	Asp	Ile	Leu	Asn	Ser	Ile	Thr	Glu	Pro	Arg	160	
145					150				155								
aga	ctc	aca	tta	ccc	ggt	atc	aac	aag	atg	cgt	caa	tgc	att	gtg	cgt	528	
Arg	Leu	Thr	Leu	Pro	Gly	Ile	Asn	Lys	Met	Arg	Gln	Cys	Ile	Val	Arg	175	
				165				170									
cta	ttg	ctt	ctc	gta	ccg	atc	caa	gta	cga	gaa	gag	atc	ctt	tct	ttc	576	
Leu	Leu	Leu	Leu	Val	Pro	Ile	Gln	Val	Arg	Glu	Glu	Ile	Leu	Ser	Phe	190	
			180					185									
gcc	ata	gct	tcg	ggg	ata	ccc	tca	gaa	aca	ata	gaa	gat	att	cga	tct	624	
Ala	Ile	Ala	Ser	Gly	Ile	Pro	Ser	Glu	Thr	Ile	Glu	Asp	Ile	Arg	Ser	205	
		195				200						205					
tca	aca	aat	att	tca	gct	gtt	gat	acc	aat	ggc	aga	ggc	ata	gca	cat	672	
Ser	Thr	Asn	Ile	Ser	Ala	Val	Asp	Thr	Asn	Gly	Arg	Gly	Ile	Ala	His	220	
	210				215						220						
aat	tcc	aaa	aag	cgg	tca	tta	gcg	cca	aca	caa	gat	tca	cgc	aat	tta	720	
Asn	Ser	Lys	Lys	Arg	Ser	Leu	Ala	Pro	Thr	Gln	Asp	Ser	Arg	Asn	Leu	240	
225					230					235							
cgc	cgt	cga	atc	agg	gga	cat	acc	caa	tag							750	
Arg	Arg	Arg	Ile	Arg	Gly	His	Thr	Gln	*								
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<210> 77

<211> 249

<212> PRT

<213> Zygosaccharomyces bailii

<400> 77

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Ala Leu Asp Leu Leu Glu Arg Leu Asp Ser Asn Trp Lys Gly Thr Glu
          20          25          30
Leu Phe Thr His Ile Arg Glu Thr Phe Gln Ile Gly Leu Gly Asn Val
          35          40          45
Ile Ile Val Ser Glu Gln Ser Glu Ser Leu Arg Ile Pro Pro Ser Leu
          50          55          60
Leu Gly Ser Ser Ser Pro Ala Asp Ser Asp Asn Ser Pro Pro Gly Thr
65          70          75          80
Pro Thr Asn Glu Ala Gln Pro Trp Phe Ile Ser Glu Asp Leu Ser Lys
          85          90          95
Gly Pro Phe Thr Glu Ala Gln Ser Thr Gln Ser Ser Ile Glu Thr Leu
          100          105          110
Glu Gly Glu His His Ala Val Ser Ser Leu His Leu Lys Leu Asn Gly
          115          120          125
Leu Ser Cys Ile Gly Arg Ala Val Trp Arg Ala Thr Arg Lys Met Asp
130          135          140
Thr Arg Thr Glu Val Asp Asp Ile Leu Asn Ser Ile Thr Glu Pro Arg
145          150          155          160
Arg Leu Thr Leu Pro Gly Ile Asn Lys Met Arg Gln Cys Ile Val Arg
          165          170          175
Leu Leu Leu Leu Val Pro Ile Gln Val Arg Glu Glu Ile Leu Ser Phe
          180          185          190
Ala Ile Ala Ser Gly Ile Pro Ser Glu Thr Ile Glu Asp Ile Arg Ser
          195          200          205
Ser Thr Asn Ile Ser Ala Val Asp Thr Asn Gly Arg Gly Ile Ala His
210          215          220
Asn Ser Lys Lys Arg Ser Leu Ala Pro Thr Gln Asp Ser Arg Asn Leu
225          230          235          240
Arg Arg Arg Ile Arg Gly His Thr Gln
          245

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<210> 78

<211> 453

<212> DNA

<213> *Saccharomyces cerevisiae*

<220>

<221> promoter

<222> (1)...(450)

<221> misc_feature

<222> (451)...(453)

<223> start codon

<400> 78

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ctacttattc ccttcgagat tataatctagg aacccatcag gttggtggaa gattaccgt 60
tctaagactt ttcagcttcc tctattgatg ttacacctgg acacccttt tctggcatcc 120
agtttttaat cttcagtggc atgtgagatt ctccgaaatt aattaaagca atcacacaat 180
tctctcggat accacctcgg ttgaaactga cagggtggtt gttacgcatg ctaatgcaaa 240
ggagcctata tacctttggc tcggctgctg taacagggaa tataaagggc agcataattt 300
aggagtttag tgaacttgca acatttacta ttttcccttc ttacgtaaat atttttcttt 360
ttaattctaa atcaatcttt ttcaattttt tgtttgtatt cttttcttgc ttaaattctat 420
aactacaaaa aacacataca taaactaaaa atg 453

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<210> 79
 <211> 499
 <212> DNA
 <213> *Zygosaccharomyces bailii*

<220>
 <221> promoter
 <222> (1)...(496)

<221> misc_feature
 <222> (497)...(499)
 <223> start codon

<400> 79
 ggatcgtatt gcttccattc ttcttttgtt attcggcgcg attcgaattc atgacatctt 60
 ttaaccgtcc gcactacatt actggctcaa gaaaggattg ataaatacta ccaaggaaca 120
 cgtgtatcca tttgatactg tgctgggttac aagacacatg ctttacaagc acacttctat 180
 ctctctcgac tgaggcgaaa cgctcgagtgg ttgatataca aatgcatgcg tgatatgcac 240
 cattatTTTT cctttttact tccgtcacgc cgggggtcca cttttttggg ttccactttt 300
 cttacgaccc tcgacatcca ctaaacgaac aggaagtcaa agaaccctc gagtcacacg 360
 gtgcgtatgc gctgttaaca tatataaagg tcacctttcc ctgctcaaaa gagtcttagc 420
 aggcgtgtaa cttcactctc tatcgatcca tagaatctaa ctaacaagag actacatcgg 480
 tataacaaat aacaaaatg 499

<210> 80
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 80
 aagagactcc aacgtcgcgc acctgta 27

<210> 81
 <211> 32
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 81
 agaggattag gaagacacaa attgcatggt ga 32

<210> 82
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR Primer

<400> 82
 atcgtattgc ttccattctt cttttgtta 29

<210> 83
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 83
tttggttattt gttataaccga tgtagtctc

29

<210> 84
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 84
tagctactct tctccagggtg tcattag

27

<210> 85
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 85
cctatgtccg agtttagcga gcttg

25

<210> 86
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 86
agaatgaact cagagttctc tcttg

25

<210> 87
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 87
attctattgg gtatgtcccc tg

22

<210> 88
<211> 30

<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 88
gtttttaatt ttgaagctca cctttaattg 30

<210> 89
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 89
attatgttct ccaggaaga ggtag 26

<210> 90
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 90
agaatcaatc atttagtgtg gcaggag 27

<210> 91
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 91
taaaaactgc ccgcatatt tcgtc 25

<210> 92
<211> 708
<212> DNA
<213> *Zygosaccharomyces rouxii*

<400> 92
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tcctctcccc ctcccctttt tttccttctt tctttccatc tatttctgat ctcctcccct 180
cagcagatgt cccgaaagggt acagctgcga tacgggcagc cactttttga cgtctcgcaa 240
caggatcacc ctgcacgacg gggcacaata ggattcccgt tggcacgggtg ctggtgtata 300
gccgcgaggg gtgggggtata aagggtaca tccttaccac cagcgaggcg ataaccgca 360
tcatacaact gtcctcctct tccgctctcg ccactagccg ccgaaccatt gctaccgcaa 420
tgacaccgtg tgggtgatctc aaggaggat gtgtgggtgt gggacggaac ttccactttt 480
tcctcagtag gtgcgatgcc ccctacaccg agcttccact aacgtgtttc agcggttgaa 540

ggcaatggga tcgcagaatt atcgcagctt gttggtatat aaagggagaa gatatatgga 600
taagagacat gttctacttc tggtctctct ttctttttat cctatatcac cagaacaaat 660
caagttcgca ttgattcata tcaaataaaa agtacatcac agataaca 708

<210> 93
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 93
tgcagaaagc cctaagatgc t 21

<210> 94
<211> 29
<212> DNA
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<220>
<223> PCR Primer

<400> 94
tgtctgtgat gtacttttta tttgatatg 29

<210> 95
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> PCR Primer

<400> 95
acgcaagaga gaactctgag ttcac 25